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OM protein - protein search, using sw model

Run on: May 3, 2004, 15:44:40 ; Search time 55 Seconds
(without alignments)
118.156 Million cell updates/sec

Title: US-09-978-178a-7
Perfect score: 116
Sequence: 1 DGDVEEERAPYEATERTTSTA 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_290a04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116	100.0	23	5	ABBB1210 Human amy
2	105.5	90.9	67	4	AAAM13864 Peptide #
3	105.5	90.9	67	4	AAAM14452 Peptide #
4	105.5	90.9	67	4	ABBB33400 Peptide #
5	105.5	90.9	67	4	ABBB2809 Peptide #
6	105.5	90.9	67	4	AAAM2865 Peptide #
7	105.5	90.9	67	4	AAAM26271 Peptide #
8	105.5	90.9	67	4	ABBB27639 Human pep
9	105.5	90.9	67	4	ABBB28225 Human pep
10	105.5	90.9	67	4	ABBB18291 Human pep
11	105.5	90.9	67	4	ABBB18859 Protein #
12	105.5	90.9	67	4	AAAM6579 Human bon
13	105.5	90.9	67	4	AAAM65995 Human bon
14	105.5	90.9	67	4	AAAM53616 Human bra
15	105.5	90.9	67	4	AAAM54185 Human bra
16	105.5	90.9	67	4	ABGG47661 Human liv
17	105.5	90.9	67	4	ABGG48247 Human liv
18	105.5	90.9	67	4	AAAM01607 Peptide #
19	105.5	90.9	67	4	AAAM02179 Peptide #
20	105.5	90.9	67	5	ABGG36231 Human pep
21	105.5	90.9	67	5	ABGG35643 Human pep
22	105.5	90.9	284	5	ABGG70914 Human sec
23	105.5	90.9	284	6	ABGG62547 Human sec
24	105.5	90.9	487	2	AAW263394 Amyloid p
25	105.5	90.9	487	2	AAW26510 Amyloid p

26	105.5	90.9	487	2	AAW42979 Amyloid p
27	105.5	90.9	487	2	AAW44745 APP-REP 7
28	105.5	90.9	492	2	AAW45229 APP-REP 7
29	105.5	90.9	492	2	AAW26393 Amyloid p
30	105.5	90.9	492	2	AAW26509 Amyloid p
31	105.5	90.9	492	2	AAW42978 Amyloid p
32	105.5	90.9	492	2	AAW44744 APP-REP 7
33	105.5	90.9	596	2	AAW65797 Beta-amy1
34	105.5	90.9	651	2	AAW65796 Beta-amy1
35	105.5	90.9	656	2	AAW58935 Amyloid p
36	105.5	90.9	670	2	AAW65795 APP751 be
37	105.5	90.9	676	2	AAW58936 Amyloid p
38	105.5	90.9	695	1	AAW81692 Sequence
39	105.5	90.9	695	2	AAW05166 Sequence
40	105.5	90.9	695	2	AAW14046 Amyloid p
41	105.5	90.9	695	2	AAW26338 APP695. 3
42	105.5	90.9	695	2	AAW58923 Mouse amy
43	105.5	90.9	695	2	AAW58920 Amyloid p
44	105.5	90.9	695	2	AAW19487 APP695 mu
45	105.5	90.9	695	2	AAW19490 APP695 mu

ALIGNMENTS

RESULT 1
ID ABBB1210 standard; peptide: 23 AA.
XX

13-AUG-2002 (first entry)

Human amyloid precursor protein derived peptide SEQ ID NO:7.

Human; amyloid precursor protein; APP; oxidative damage; vasotropic; neurotropic; cardiac; cellular injury; oxidative stress; stroke; heart attack; spinal injury; Alzheimer's disease; nerve cell growth; iron-catalysed oxidative damage; nerve cell regeneration.

OS Homo sapiens.

PN WO200234766-A2.

PD 02-MAY-2002.

PF 24-OCT-2001; 2001WO-US032627.

PR 27-OCT-2000; 2000US-023403P.

PR 17-OCT-2001; 2001US-00978178.

PA (BGM) BRIGHAM & WOMENS HOSPITAL INC.

PT Rogers J;

DR WPI; 2002-471430/50.

XX New peptides derived from human amyloid precursor protein, useful in protecting human cells from oxidative damage, and for reducing oxidation-related damage in a patient suffering from stroke or heart attack.

XX Claim 6; Page 11; 16pp; English.

XX The present invention describes a peptide (I) that corresponds to CC segments (such as ferrocholate sequence homology domain (FOX-1) and FOX-2) within human Alzheimer's amyloid precursor protein (APP) (referred as APP -695), and which is useful in protecting human cells from oxidative damage. (I) has vasotropic, neurotropic and cardiac activities, and reduces or prevents cellular injury resulting from oxidative stress. (I) is useful for protecting human cells e.g. vascular smooth muscle cells, CC vascular endothelial cells or neuronal cells. Pharmaceutical compositions CC comprising (I) can be used for reducing oxidation-related damage in a CC patient suffering from a stroke, heart attack or spinal injury and

CC preventing stress-related cellular injury in a patient undergoing
CC surgery. (1) is most preferably useful for protecting cells from iron-
CC catalyzed oxidative damage. (1) is useful for optimizing conditions for
CC nerve cell growth and regeneration after stroke, heart attack or spinal
CC injury. (1) is also useful for preventing reperfusion injuries associated
CC with stroke, heart attack, or spinal injury. The present sequence
CC represents a specifically claimed human APP derived peptide from the
CC present invention
XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 116; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DGDVEEERAEPEATEERTTSTA 23
1 DGDVEEERAEPEATEERTTSTA 23

Db 1 DGDVEEERAEPEATEERTTSTA 23

RESULT 2

AA013864 standard; protein; 67 AA.

AA013864;

12-OCT-2001 (first entry)

Peptide #298 encoded by probe for measuring cervical gene expression.

Probe; human; microarray; gene expression; cervical epithelial cell;

cervical cancer.

Homo sapiens.

MO200157278-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US000670.

04-FEB-2000; 2000US-0180312P.

26-MAY-2000; 2000US-0207456P.

30-JUN-2000; 2000US-00608408.

03-AUG-2000; 2000US-00632366.

21-SEP-2000; 2000US-0234687P.

27-SEP-2000; 2000US-0236359P.

04-OCT-2000; 2000GB-00024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-488901/53.

Claim 27; SEQ ID NO 18690; 487pp; English.

The present invention relates to human single exon nucleic acid probes
(SNP: see A110068-A128459). The present sequence is a peptide encoded
by one such probe. The SNPs are derived from human Hela cells. The SNPs
can be used to produce a single exon microarray, which can be used for
measuring human gene expression in a sample derived from human cervical
epithelial cells. By measuring gene expression, the probes are therefore
useful in grading and/or staging of diseases of the cervix, notably
cervical cancer. Note: The sequence data for this patent did not form
part of the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
Sequence 67 AA;

Query Match 90.9%; Score 105.5; DB 4; Length 67;
Best Local Similarity 95.8%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 DGDVEEERAEPEATEERTTSTA 23
29 DGDVEEERAEPEATEERTTSTA 52

Db 29 DGDVEEERAEPEATEERTTSTA 52

RESULT 3

AA014452 standard; protein; 67 AA.

AA014452;

12-OCT-2001 (first entry)

Peptide #886 encoded by probe for measuring cervical gene expression.

Probe; human; microarray; gene expression; cervical epithelial cell;

cervical cancer.

Homo sapiens.

MO200157278-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US000670.

04-FEB-2000; 2000US-0180312P.

26-MAY-2000; 2000US-0207456P.

30-JUN-2000; 2000US-00608408.

03-AUG-2000; 2000US-00632366.

21-SEP-2000; 2000US-0234687P.

27-SEP-2000; 2000US-0236359P.

04-OCT-2000; 2000GB-00024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-488901/53.

Claim 27; SEQ ID NO 19278; 487pp; English.

The present invention relates to human single exon nucleic acid probes
(SNP: see A110068-A128459). The present sequence is a peptide encoded
by one such probe. The SNPs are derived from human Hela cells. The SNPs
can be used to produce a single exon microarray, which can be used for
measuring human gene expression in a sample derived from human cervical
epithelial cells. By measuring gene expression, the probes are therefore
useful in grading and/or staging of diseases of the cervix, notably
cervical cancer. Note: The sequence data for this patent did not form
part of the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
Sequence 67 AA;

Query Match 90.9%; Score 105.5; DB 4; Length 67;
Best Local Similarity 95.8%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 DGDVEEERAEPEATEERTTSTA 23
29 DGDVEEERAEPEATEERTTSTA 52

Db 29 DGDVEEERAEPEATEERTTSTA 52

RESULT 4

AB033400

ID ABB33400 standard; peptide; 67 AA.
XX ABB33400;
XX
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #906 encoded by human foetal liver single exon probe.
XX
XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001MO-US000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
PS Claim 27; SEQ ID NO 26035; 639pp + Sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 67 AA;
XX
Query Match 90.9%; Score 105.5; DB 4; Length 67;
Best Local Similarity 95.8%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
QY 1 DGDEVEEBA-EPYEATERRTTSTA 23
Db 29 DGDEVEEBAEPYEATERRTTSTA 52
XX
RESULT 5
ABB32809
ID ABB32809 standard; peptide; 67 AA.
XX
XX ABB32809;
XX
XX 04-FEB-2002 (first entry)
XX
XX Peptide #15 encoded by human foetal liver single exon probe.
XX
XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
XX Homo sapiens.
XX
XX WO200157277-A2.
XX

PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001MO-US000669.
XX
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
PS Claim 27; SEQ ID NO 25444; 639pp + Sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 67 AA;
XX
Query Match 90.9%; Score 105.5; DB 4; Length 67;
Best Local Similarity 95.8%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
QY 1 DGDEVEEBA-EPYEATERRTTSTA 23
Db 29 DGDEVEEBAEPYEATERRTTSTA 52
XX
RESULT 6
AAM26865
ID AAM26865 standard; protein; 67 AA.
XX
XX AAM26865;
XX
XX 17-OCT-2001 (first entry)
XX
XX Peptide #902 encoded by probe for measuring placental gene expression.
XX
XX Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200157272-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001MO-US000663.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX

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XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
DR Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
XX Claim 27; SEQ ID NO 27134; 654bp; English.
PS
CC The present invention relates to single exon nucleic acid probes (SENP:
CC see AAI131315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
XX Sequence 67 AA:
SQ
Query Match          90.9%; Score 105.5; DB 4; Length 67;
Best Local Similarity 95.8%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Cy      1 DGDVEVEEBA-EPYEATEERTTSTA 23
Db      29 DGDVEVEEBAEPYEATEERTTSTA 52

RESULT 7
AAI26271
ID AAI26271 standard; protein; 67 AA.
XX
XX AAI26271;
AC
XX 17-OCT-2001 (first entry)
DT
XX Peptide #308 encoded by probe for measuring placental gene expression.
DE
XX Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.
XX
XX Homo sapiens.
OS
XX WO200157272-A2.
PN
XX 09-AUG-2001.
PD
XX 30-JAN-2001; 2001WO-US000663.
PF
XX 04-FEB-2000; 2000US-0180312P.
PR
XX 26-MAY-2000; 2000US-0207456P.
PT
XX 30-JUN-2000; 2000US-00608408.
PR
XX 03-AUG-2000; 2000US-00632366.
PR
XX 21-SEP-2000; 2000US-0234687P.
PR
XX 27-SEP-2000; 2000US-0236359P.
PR
XX 04-OCT-2000; 2000GB-00024263.
PA
XX (MOLE-) MOLECULAR DYNAMICS INC.
PI
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
DR
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
XX Claim 27; SEQ ID NO 26540; 654bp; English.
PS
CC The present invention relates to single exon nucleic acid probes (SENP:
CC see AAI131315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of

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CC human genetic disorders
XX
XX Sequence 67 AA;
SQ
Query Match          90.9%; Score 105.5; DB 4; Length 67;
Best Local Similarity 95.8%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Cy      1 DGDVEVEEBA-EPYEATEERTTSTA 23
Db      29 DGDVEVEEBAEPYEATEERTTSTA 52

RESULT 8
ABB27639
ID ABB27639 standard; peptide; 67 AA.
XX
XX ABB27639;
AC
XX 01-FEB-2002 (first entry)
DT
XX Human peptide #290 encoded by breast cell single exon nucleic acid probe.
DE
XX Human; microarray; single exon probe; gene expression; breast; disease;
XX cancer.
XX
XX Homo sapiens.
OS
XX WO200157271-A2.
PN
XX 09-AUG-2001.
PD
XX 30-JAN-2001; 2001WO-US000662.
PF
XX 04-FEB-2000; 2000US-0180312P.
PR
XX 26-MAY-2000; 2000US-0207456P.
PT
XX 30-JUN-2000; 2000US-00608408.
PR
XX 03-AUG-2000; 2000US-00632366.
PR
XX 21-SEP-2000; 2000US-0234687P.
PR
XX 27-SEP-2000; 2000US-0236359P.
PR
XX 04-OCT-2000; 2000GB-00024263.
PA
XX (MOLE-) MOLECULAR DYNAMICS INC.
PI
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/54.
DR
XX New spatially-addressable set of single exon nucleic acid probes, useful
PT for measuring gene expression in sample derived from human breast,
PT comprises number of single exon nucleic acid probes.
XX
XX Claim 27; SEQ ID NO 10607; 327bp + Sequence Listing; English.
PS
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting the
CC probes with a collection of detectably labelled nucleic acids derived
CC from mRNA of human breast, and then measuring the label bound to each
CC probe of the microarray. The probes are useful for verifying the
CC expression of regions of genomic DNA predicted to encode proteins. They
CC are useful for gene discovery, and for determining predisposition and/or
CC prognosing breast disease. Gene expression analysis is useful for
CC assessing the toxicity of chemical agents on cells. The microarray of
CC this invention presents a far greater diversity of probes for measuring
CC gene expression, with far less bias than expressed sequence tag
CC microarrays. The method is suitable for rapid production of functional
CC information from genomic sequence. The present sequence is a peptide
CC encoded by a single exon nucleic acid probe of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX

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SQL Sequence 67 AA;

Query Match 90.9%; Score 105.5; DB 4; Length 67;
Best Local Similarity 95.8%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 DGDEVEEER-EPYEATERITSIA 23
DB 29 DGDEVEEER-EPYEATERITSIA 52

RESULT 9
ABB28225
ID ABB28225 standard; peptide; 67 AA.
XX ABB28225;
AC ABB28225;
DT 01-FEB-2002 (first entry)
XX
XX Human peptide #876 encoded by breast cell single exon nucleic acid probe.
XX Human; microarray; single exon probe; gene expression; breast; disease;
XX cancer.
XX Homo sapiens.
XX WO200157271-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001MO-US000662.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-496933/54.
XX
XX New spatially-addressable set of single exon nucleic acid probes, useful
XX for measuring gene expression in sample derived from human breast,
XX comprises number of single exon nucleic acid probes.
XX
XX Claim 27; SEQ ID NO 11193; 327pp + Sequence Listing; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human breast and BT 474 cells. The method involves contacting the
XX probes with a collection of detectably labelled nucleic acids derived
XX from mRNA of human breast, and then measuring the label bound to each
XX probe of the microarray. The probes are useful for verifying the
XX expression of regions of genomic DNA predicted to encode proteins. They
XX are useful for gene discovery, and for determining predisposition and/or
XX prognosing breast disease. Gene expression analysis is useful for
XX assessing the toxicity of chemical agents on cells. The microarray of
XX this invention presents a far greater diversity of probes for measuring
XX gene expression, with far less bias than expressed sequence tag
XX microarrays. The method is suitable for rapid production of functional
XX information from genomic sequence. The present sequence is a peptide
XX encoded by a single exon nucleic acid probe of the invention. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 67 AA;

Query Match 90.9%; Score 105.5; DB 4; Length 67;
Best Local Similarity 95.8%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 DGDEVEEER-EPYEATERITSIA 23
DB 29 DGDEVEEER-EPYEATERITSIA 52

RESULT 10
ABB18291
ID ABB18291 standard; protein; 67 AA.
XX ABB18291;
AC ABB18291;
DT 23-JAN-2002 (first entry)
XX
XX Protein #290 encoded by probe for measuring heart cell gene expression.
XX Human; gene expression; heart; microarray; vascular system;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease.
XX Homo sapiens.
XX WO200157274-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001MO-US000666.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts.
XX
XX Claim 15; SEQ ID NO 20061; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring gene expression in a sample derived from human heart (see
XX ABB21535-ABM41305). The present sequence is a protein encoded by one such
XX probe. The probes may be used for predicting, measuring and displaying
XX gene expression in samples derived from the human heart via microarrays.
XX By measuring gene expression, the probes are useful for predicting,
XX diagnosing, grading, staging, monitoring and prognosing diseases of the
XX human heart and vascular system e.g. cardiovascular disease,
XX hypertension, cardiac arrhythmias and congenital heart disease.
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 67 AA;

Query Match 90.9%; Score 105.5; DB 4; Length 67;
Best Local Similarity 95.8%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 DGDEVEEER-EPYEATERITSIA 23
DB 29 DGDEVEEER-EPYEATERITSIA 52

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RESULT 11
AB18859
ID AB18859 standard; protein; 67 AA.
XX
XX
AC AB18859;
XX
XX
DT 23-JAN-2002 (first entry)
XX
DE Protein #858 encoded by probe for measuring heart cell gene expression.
XX
XX
KW Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200157274-A2.
XX
XX
PD 09-AUG-2001.
XX
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX
WPI; 2001-488990/53.
XX
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
XX
XX
PS Claim 15; SEQ ID NO 20629; 530pp; English.
XX
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41105). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ffp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 67 AA;
XX
XX
Query Match 90.9%; Score 105.5; DB 4; Length 67;
Best Local Similarity 95.8%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
QY 1 DGDVEEER-EPYBEATERTTSTA 23
Db 29 DGDVEEER-EPYBEATERTTSTA 52
XX
XX
RESULT 12
AAM6579
ID AAM6579 standard; protein; 67 AA.
XX
XX
AC AAM6579;
XX
XX
DT 06-NOV-2001 (first entry)
```

```
XX
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26885.
XX
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200157276-A2.
XX
XX
PD 09-AUG-2001.
XX
XX
PF 30-JAN-2001; 2001WO-US000668.
XX
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX
WPI; 2001-488990/53.
XX
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX
XX
PS Example 4; SEQ ID NO 26885; 658bp + Sequence listing; English.
XX
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention
XX
XX
SQ Sequence 67 AA;
XX
XX
Query Match 90.9%; Score 105.5; DB 4; Length 67;
Best Local Similarity 95.8%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
QY 1 DGDVEEER-EPYBEATERTTSTA 23
Db 29 DGDVEEER-EPYBEATERTTSTA 52
XX
XX
RESULT 13
AAM65995
ID AAM65995 standard; protein; 67 AA.
XX
XX
AC AAM65995;
XX
XX
DT 06-NOV-2001 (first entry)
XX
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26301.
XX
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200157276-A2.
XX
XX
PD 09-AUG-2001.
XX
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PF 30-JAN-2001; 2001WO-US000668.
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PR 04-FEB-2000; 2000US-0180312P.
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PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX
XX Example 4; SEQ ID NO 26301; 658bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention
CC
XX
SQ Sequence 67 AA;

Query Match 90.9%; Score 105.5; DB 4; Length 67;
Best Local Similarity 95.8%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 DGDVEBEA-EPYEATERTTSIA 23
Db 29 DGDVEBEAEPYEATERTTSIA 52

RESULT 14

AAM53616
ID AAM53616 standard; protein; 67 AA.

XX AAM53616;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 25721.

XX Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

XX Homo sapiens.

OS WO200157275-A2.

XX WO200157275-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000667.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.

XX Example 4; SEQ ID NO 25721; 650bp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
CC
XX
SQ Sequence 67 AA;

Query Match 90.9%; Score 105.5; DB 4; Length 67;
Best Local Similarity 95.8%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 DGDVEBEA-EPYEATERTTSIA 23
Db 29 DGDVEBEAEPYEATERTTSIA 52

RESULT 15

AAM54185
ID AAM54185 standard; protein; 67 AA.

XX AAM54185;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 26290.

XX Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

XX Homo sapiens.

OS WO200157275-A2.

XX WO200157275-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000667.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human

PT brains.

XX Example 4; SEQ ID NO 26290; 650bp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
CC
XX
SQ Sequence 67 AA;

Query Match 90.9%; Score 105.5; DB 4; Length 67;

Best local Similarity 95.8%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 DGDVEEEA-EPYEATERRTSIA 23
Db 29 DGDVEEEAEPYEATERRTSIA 52

Search completed: May 3, 2004, 16:09:07
Job time : 57 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2004, 16:08:05 ; Search time 23 Seconds
(without alignments)
51.626 Million cell updates/sec

Title: US-09-978-178a-7

Perfect score: 116

Sequence: 1 DGDVEEBAEPYEATERTTSTA 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/2/1aa/6A-COMB.pep.*
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6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	105.5	90.9	120	6 5218100-6	Patent No. 5218100
2	105.5	90.9	284	4 US-09-141-951-1	Sequence 1, Appli
3	105.5	90.9	487	1 US-08-462-859A-9	Sequence 9, Appli
4	105.5	90.9	487	1 US-08-123-659A-9	Sequence 9, Appli
5	105.5	90.9	487	1 US-08-464-247A-9	Sequence 9, Appli
6	105.5	90.9	487	1 US-08-464-248A-9	Sequence 9, Appli
7	105.5	90.9	492	1 US-08-462-859A-7	Sequence 7, Appli
8	105.5	90.9	492	1 US-08-123-659A-7	Sequence 7, Appli
9	105.5	90.9	492	1 US-08-464-247A-7	Sequence 7, Appli
10	105.5	90.9	492	1 US-08-464-248A-7	Sequence 7, Appli
11	105.5	90.9	656	1 US-08-371-930-23	Sequence 23, Appli
12	105.5	90.9	656	1 PCT-US94-01712-23	Sequence 23, Appli
13	105.5	90.9	676	1 US-08-371-930-24	Sequence 24, Appli
14	105.5	90.9	676	1 PCT-US94-01712-24	Sequence 24, Appli
15	105.5	90.9	694	1 US-08-339-152A-18	Sequence 18, Appli
16	105.5	90.9	694	2 US-08-007-999B-5	Sequence 5, Appli
17	105.5	90.9	694	2 US-08-689-276A-5	Sequence 5, Appli
18	105.5	90.9	695	1 US-08-371-930-27	Sequence 27, Appli
19	105.5	90.9	695	1 US-08-123-702-2	Sequence 2, Appli
20	105.5	90.9	695	1 US-08-339-152A-30	Sequence 30, Appli
21	105.5	90.9	695	2 US-08-104-165-1	Sequence 1, Appli
22	105.5	90.9	695	3 US-08-464-250-1	Sequence 1, Appli
23	105.5	90.9	695	4 US-08-464-250-1	Sequence 1, Appli
24	105.5	90.9	695	4 US-09-458-481B-6	Sequence 6, Appli
25	105.5	90.9	695	4 US-09-458-481B-7	Sequence 7, Appli
26	105.5	90.9	695	4 US-09-458-481B-8	Sequence 8, Appli
27	105.5	90.9	695	4 US-09-548-372D-10	Sequence 10, Appli

28	105.5	90.9	695	4 US-09-548-372D-12	Sequence 12, Appli
29	105.5	90.9	695	4 US-09-548-372D-14	Sequence 14, Appli
30	105.5	90.9	695	4 US-09-548-367D-10	Sequence 10, Appli
31	105.5	90.9	695	4 US-09-548-367D-12	Sequence 12, Appli
32	105.5	90.9	695	4 US-09-548-367D-14	Sequence 14, Appli
33	105.5	90.9	695	4 US-09-551-853D-10	Sequence 10, Appli
34	105.5	90.9	695	4 US-09-551-853D-12	Sequence 12, Appli
35	105.5	90.9	695	4 US-09-551-853D-14	Sequence 14, Appli
36	105.5	90.9	695	4 US-09-415-099-6	Sequence 6, Appli
37	105.5	90.9	695	4 PCT-US94-01712-27	Sequence 27, Appli
38	105.5	90.9	695	6 5218100-2	Patent No. 5218100
39	105.5	90.9	697	4 US-09-548-372D-16	Sequence 16, Appli
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42	105.5	90.9	697	4 US-09-548-367D-16	Sequence 16, Appli
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44	105.5	90.9	697	4 US-09-548-367D-20	Sequence 20, Appli
45	105.5	90.9	697	4 US-09-551-853D-16	Sequence 16, Appli

ALIGNMENTS

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RESULT 1
5218100-6
; Patent No. 5218100
; APPLICANT: MILLER-HILL, BENNO;KANG, JIE;LEMAIRE, HANS-GEORG;
; UNTERBECK, AXEL
; TITLE OF INVENTION: DNA ENCODING FOR THE PRECURSOR PROTEIN
; OF APC POLYPEPTIDE ASSOCIATED WITH ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/144,297
; FILING DATE: 15-JUN-1988
; SEQ ID NO: 6
; LENGTH: 120
5218100-6

Query Match          90.9%; Score 105.5; DB 6; Length 120;
Best Local Similarity 95.8%; Pred. No. 6.1e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 DGDVEEBAEPYEATERTTSTA 23
DB 70 DGDVEEBAEPYEATERTTSTA 93

RESULT 2
US-09-141-951-1
; Sequence 1, Application US/09141951A
; Patent No. 6440678
; GENERAL INFORMATION:
; APPLICANT: Barger, Steven W.
; TITLE OF INVENTION: Materials and Methods Related to the Inflammatory
; FILE REFERENCE: P-1048
; CURRENT APPLICATION NUMBER: US/09/141,951A
; CURRENT FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-141-951-1

Query Match          90.9%; Score 105.5; DB 4; Length 284;
Best Local Similarity 95.8%; Pred. No. 1.6e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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RESULT 3
US-08-462-859A-9
Sequence 9, Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: No. 5652092a1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-9
Query Match 90.9%; Score 105.5; DB 1; Length 487;
Best Local Similarity 95.8%; Pred. No. 2.9e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
OY 1 DGDVEEBA-EPEEATERTTSIA 23
Db 250 DGDVEEBAEPEEATERTTSIA 273
RESULT 4
US-08-123-659A-9
Sequence 9, Application US/08123659A
Patent No. 566477
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: No. 566477e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-9
Query Match 90.9%; Score 105.5; DB 1; Length 487;
Best Local Similarity 95.8%; Pred. No. 2.9e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
OY 1 DGDVEEBA-EPEEATERTTSIA 23
Db 250 DGDVEEBAEPEEATERTTSIA 273
RESULT 5
US-08-464-247A-9
Sequence 9, Application US/08464247A
Patent No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-9

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 16:10:31 ; Search time 42 Seconds

(Without alignments)
151.794 Million cell updates/sec

Title: US-09-978-178a-7

Perfect score: 116
Sequence: 1 DGDVEERAEPEAEATERTSIA 23

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Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	105.5	90.9	67	9	US-09-864-761-33589
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4	105.5	90.9	284	14	US-10-166-482A-1
5	105.5	90.9	695	9	US-09-794-927-10
6	105.5	90.9	695	9	US-09-794-927-12
7	105.5	90.9	695	9	US-09-794-927-14
8	105.5	90.9	695	9	US-09-795-847-10
9	105.5	90.9	695	9	US-09-795-847-12
10	105.5	90.9	695	9	US-09-795-847-14
11	105.5	90.9	695	9	US-09-794-743-10
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16	105.5	90.9	695	9	US-09-794-748-14	Sequence 14, Appl
17	105.5	90.9	695	9	US-09-794-925-10	Sequence 10, Appl
18	105.5	90.9	695	9	US-09-794-925-12	Sequence 12, Appl
19	105.5	90.9	695	9	US-09-794-925-14	Sequence 14, Appl
20	105.5	90.9	695	9	US-09-681-442-10	Sequence 10, Appl
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ALIGNMENTS

RESULT 1
US-09-978-178-7
; Sequence 7, Application US/09978178
; Publication No. US20030004101A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Jack
; TITLE OF INVENTION: Peptides Derived from the Human Amyloid Precursor Protein
; FILE REFERENCE: 7570/73272
; CURRENT APPLICATION NUMBER: US/09/978,178
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-178-7
Query Match 100.0%; Score 116; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-09-864-761-33589
; Sequence 33589, A
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
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PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/224,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33589
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 20
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 22
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 14
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OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 16
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 15
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 13
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 15
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 16
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 20
US-09-864-761-33589
Query Match 90.9%; Score 105.5; DB 9; Length 67;
Best Local Similarity 95.8%; Pred. No. 1e-06;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 29 DGDVEEBAEPEYEATERTTSTA 52

QY 1 DGDVEEBAEPEYEATERTTSTA 23

RESULT 3
US-09-864-761-34157
Sequence 34157, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 34157
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AP000089.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.3
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 8.7
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 8.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
US-09-864-761-34157
Query Match 90.9%; Score 105.5; DB 9; Length 67;
Best Local Similarity 95.8%; Pred. No. 1e-06;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 29 DGDVEEBAEPEYEATERTTSTA 52

QY 1 DGDVEEBAEPEYEATERTTSTA 23

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OM protein - protein search, using sw model

Run on: May 3, 2004, 16:09:11 ; Search time 181 Seconds

(without alignments)
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Title: US-09-978-178a-7

Perfect score: 116
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Listing first 45 summaries

Database :

Pending Patents, AA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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4	105.5	90.9	67	23	US-09-864-761-34157	Sequence 34157, A	
5	105.5	90.9	67	27	US-10-182-993-25721	Sequence 25721, A	
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44	105.5	90.9	695	1	PCT-US01-00797-10	Sequence 10, Appli	
45	105.5	90.9	695	1	PCT-US01-00797-12	Sequence 12, Appli	

ALIGNMENTS

RESULT 1
US-09-978-178-7
; Sequence 7, Application US/09978178
; GENERAL INFORMATION:
; APPLICANT: Rogers, Jack
; TITLE OF INVENTION: Peptides Derived from the Human Amyloid Precursor Protein
; FILE REFERENCE: 7570/73372
; CURRENT APPLICATION NUMBER: US/09/978,178
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-178-7

Query Match 100.0%, Score 116, DB 25, Length 23;
Best local Similarity 100.0%; Pred. No. 2e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DGDVEEAEAPYEATERTTSIA 23
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Db 1 DGDVEBEAEPEYEATERRTSIA 23

RESULT 2

PCT-US01-00663-26540

Sequence 26540, Application PC/TUS0100663

GENERAL INFORMATION:

APPLICANT: Molecular Dynamics, Inc.

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA

FILE REFERENCE: PB 0004 WO 7

CURRENT APPLICATION NUMBER: PCT/US01/00663

CURRENT FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 04 February 2000 (04.02.00)

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 26 May 2000 (26.05.00)

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 03 August 2000 (03.08.00)

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 03 October 2000 (03.10.00)

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 30 June 2000 (30.06.00)

NUMBER OF SEQ ID NOS: 38837

SOFTWARE: Molecular Dynamics Sequence Listing Engine

SEQ ID NO 26540

LENGTH: 67

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AP000142.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 15

PCT-US01-00663-26540

Query Match

Best Local Similarity 90.9%; Score 105.5; DB 1; Length 67;

Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 29 DGDVEBEAEPEYEATERRTSIA 52

RESULT 3

PCT-US01-00663-27134

Sequence 27134, Application PC/TUS0100663

GENERAL INFORMATION:

APPLICANT: Molecular Dynamics, Inc.

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA

FILE REFERENCE: PB 0004 WO 7

CURRENT APPLICATION NUMBER: PCT/US01/00663

CURRENT FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 04 February 2000 (04.02.00)

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 26 May 2000 (26.05.00)

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 03 August 2000 (03.08.00)

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 03 October 2000 (03.10.00)

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 30 June 2000 (30.06.00)

NUMBER OF SEQ ID NOS: 38837

SOFTWARE: Molecular Dynamics Sequence Listing Engine

SEQ ID NO 27134

LENGTH: 67

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AP000089.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.3

PCT-US01-00663-27134

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Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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RESULT 4

US-09-864-761-33589

Sequence 33589, Application US/09864761

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Aeomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 16:07:00 ; Search time 21 Seconds
(without alignments)

105.353 Million cell updates/sec

Title: US-09-978-178a-7

Perfect score: 116

Sequence: 1 DGDVEEAEAEPEEATERTTSTA 23

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105.5	90.9	484	4 A32761	hypothetical Alzhe
2	105.5	90.9	695	1 A49795	Alzheimer's diseas
3	105.5	90.9	695	2 S00550	Alzheimer's diseas
4	105.5	90.9	770	1 QRH044	Alzheimer's diseas
5	100.5	86.6	695	2 A27485	Alzheimer's diseas
6	96.5	83.2	747	2 JH0773	Alzheimer's diseas
7	56	48.3	414	2 S33659	55K antigen - Pneu
8	53	45.7	417	2 T20327	hypothetical prote
9	53	45.7	519	1 S78850	petit2 protein - S
10	52	44.8	738	2 S37876	glutamine-rich pro
11	52	44.8	798	2 T33022	hypothetical prote
12	52	44.8	866	2 B85075	probable achilla tr
13	51	44.0	309	2 H70381	ferrochelatase (EC
14	51	44.0	325	2 JCS276	HXC-26 protein - h
15	51	44.0	361	2 S68268	apurinic/aprimidi
16	51	44.0	455	2 T40940	hypothetical prote
17	50	43.1	189	2 C83936	hypothetical prote
18	50	43.1	197	2 T02062	hypothetical prote
19	50	43.1	897	2 T21688	hypothetical prote
20	49	42.2	606	2 S70358	centromere protein
21	49	42.2	671	2 S53407	CHS5 protein - yea
22	49	42.2	699	2 T01029	hypothetical prote
23	49	42.2	1182	2 T30189	myelin transcripti
24	49	42.2	1188	2 T46608	zinc finger protei
25	49	42.2	3283	2 AC1018	large repetitive p
26	48.5	41.8	861	2 S77409	hypothetical prote
27	48	41.4	191	2 T31876	hypothetical prote
28	48	41.4	300	2 T01588	hypothetical prote
29	48	41.4	407	1 EDBE03	immediate-early pr

30	48	41.4	924	1 S27421	cell division cont
31	48	41.4	5170	2 T15348	hypothetical prote
32	47.5	40.9	297	2 H04186	hypothetical prote
33	47.5	40.9	364	2 JCS529	p38 beta2 mitogen
34	47.5	40.9	372	2 G02524	MAP kinase (BC 2.7
35	47	40.5	477	2 T46125	calmodulin-binding
36	47	40.5	533	2 A57180	chromogranin/secre
37	47	40.5	538	2 A54391	translation initia
38	47	40.5	544	2 B44841	low molecularweig
39	47	40.5	587	2 JCS300	Ran GTPase activat
40	47	40.5	760	2 T24521	hypothetical prote
41	47	40.5	881	2 AE2777	potassium efflux s
42	47	40.5	881	2 B97557	hypothetical prote
43	47	40.5	965	2 T50670	actin bundling pro
44	47	40.5	1664	2 F84485	probable retrolem
45	47	40.5	2513	2 G96536	hypothetical prote

ALIGNMENTS

RESULT 1

A32761
Hypothetical Alzheimer's disease amyloid beta protein, Alu-containing clone - human (fr
C/Species: Homo sapiens (man)
C/Date: 29-Jan-1990 #sequence_revision 10-Apr-1996 #text_change 10-Apr-1996
C/Accession: A32761
R/de Sauvage, F.; Octave, J.N.
Science 245, 651-653, 1989
A/Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secreted F
A/Reference number: A32761; MUID:89346754; PMID:2569763
A/Accession: A32761
A/Molecule type: mRNA
A/Residues: 1-484 <DBS>
A/Cross-references: GB:M28373
A/Note: the authors translated the codon ATG for residue 433 as Leu
C/Comment: This is the hypothetical translation of a sequence believed to contain clon
C/Keywords: cloning artifact

Query Match

Best local Similarity 90.9%; Score 105.5; DB 4; Length 484;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 DGDVEEAEAEPEEATERTTSTA 23

DB 171 DGDVEEAEAEPEEATERTTSTA 194

RESULT 2

A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C/Species: Macaca fascicularis (crab-eating macaque)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: A49795
R/Podlasky, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A/Title: Homology of the amyloid beta protein precursor in monkey and human supports a
A/Reference number: A49795; MUID:91273117; PMID:1905108
A/Accession: A49795
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-695 <POD>
A/Cross-references: GB:M58727; NID:G342062; PIDN:AAA36829.1; PID:G342063
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-Lyze proteinase
C/Keywords: alternative splicing

Query Match

Best local Similarity 90.9%; Score 105.5; DB 1; Length 695;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 DGDVEEAEAEPEEATERTTSTA 23
DB 250 DGDVEEAEAEPEEATERTTSTA 273

RESULT 3

S00550

Alzheimer's disease amyloid beta protein precursor - rat
 N:Alternate names: beta-A4 amyloid protein
 C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 13-Aug-1999

C:Accession: S00550; A41245; A39820; S46251
 R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
 EMO J. 7, 1365-1370, 1988

A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
 A:Reference number: S00550; PMID:88312583; PMID:2900758

A:Accession: S00550

A:Molecule type: mRNA

A:Residues: 1-695 <SH1>

A:Cross-references: EMBL:X07648; NID:G55616; PIDD:CAA30488.1; PID:G55617

R:Schubert, D.; Schroeder, R.; LaCorbiere, M.; Salton, T.; Cole, G.

Science 241, 223-226, 1988
 A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core

A:Reference number: A41245; PMID:88264430; PMID:2568652

A:Accession: A41245

A:Molecule type: protein

A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>

A:Note: evidence for heparan sulfate attachment

R:Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.

FEBS Lett. 349, 109-116, 1994

A:Title: The beta-A4 amyloid precursor protein binding to copper.

A:Reference number: S46251; PMID:94320627; PMID:7913895

A:Contents: annotation; copper binding sites

A:Note: rat peptides were isolated but not sequenced

R:Potempa, A.; Styles, J.; Mehra, P.; Kim, K.S.; Miller, D.L.

J. Biol. Chem. 266, 8464-8469, 1991

A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain

A:Reference number: A39820; PMID:9121087; PMID:1673661

A:Accession: A39820

A:Status: preliminary

A:Molecule type: protein

A:Residues: 18-32 <POT>

A:Experimental source: brain

C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Knutiz-type proteinase 1

F:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein

F:625-648/Domain: transmembrane #status predicted <TM>

Query Match 90.9%; Score 105.5; DB 2; Length 625;
 Best Local Similarity 95.8%; Pred. No. 1.3e-06;
 Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

1 DGDVEEEREA-EPYEATERTTSTA 23
 250 DGDVEEEREAEPYEATERTTSTA 273

RESULT 4

OR01A4

Alzheimer's disease amyloid beta protein precursor [validated] - human
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibitor; Contains: amyloid beta protein long; plaque form; amyloid beta protein short; vascular protein precursor splice form APP(770)

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence revision 28-Jul-1995 #text_change 15-Sep-2000
 C:Accession: S02260; S05194; A32277; A33260; A35486; I39451; I39453; I59562; A44

4668; A28583; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S29076; S38252; S3

R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey

Nucleic Acids Res. 17, 517-522, 1989

A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b

A:Reference number: S02260; PMID:89128427; PMID:2783775

A:Accession: S02260

A:Molecule type: DNA

A:Residues: 1-288, 'V', 365-770 <LEM1>

A:Cross-references: EMBL:X13466
 A:Note: alternative splice form APP (695)

R:Lemaire, H.G.

submitted to the EMBL Data Library, November 1988

A:Reference number: S05194

A:Accession: S05194

A:Molecule type: DNA

A:Residues: 1-14, 'W', 17-288, 'V', 365-770 <LEM2>

A:Cross-references: EMBL:X13466; NID:G35598; PIDD:CAA31830.1; PID:G871360

A:Note: alternative splice form APP(695)

R:La Raut, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.

Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote

A:Reference number: A32277; PMID:89165870; PMID:2538123

A:Accession: A32277

A:Molecule type: DNA

A:Residues: 1-75 <LA>

A:Cross-references: GB:M24546; GB:M24547; NID:G341202; PIDD:AACT3654.1; PID:G516074

R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.

Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit

A:Reference number: A33260; PMID:89392030; PMID:2675837

A:Accession: A33260

A:Molecule type: DNA

A:Residues: 656-737 <JOH>

A:Cross-references: GB:M23270; NID:G178863; PIDD:AAAS1768.1; PID:G178865

R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Prangione, B.

Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of

A:Reference number: A35486; PMID:90321244; PMID:2196878

A:Accession: A35486

A:Molecule type: DNA

A:Residues: 672-710 <PRE1>

A:Note: 693-oln was found in DNA isolated from HCHWA-D patients

R:Koshtak, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.

Gene 87, 257-263, 1990
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.

A:Reference number: I39451; PMID:90236318; PMID:2110105

A:Accession: I39451

A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMB

A:Molecule type: DNA

A:Residues: 1-770 <YOS1>

A:Cross-references: GB:M33112; NID:G178613; PIDD:AAAS9502.1; PID:G178616

A:Accession: I39451

A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMB

A:Molecule type: DNA

A:Residues: 1-530, 'OMLMPVTPAPWEAKYGR' <YOS2>

A:Cross-references: GB:M34875; NID:G178608; PIDD:AAAS9501.1; PID:G178615

R:Koshikata, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.

Gene 102, 291-292, 1991
 A:Reference number: A59020; PMID:91340168; PMID:1908403

A:Contents: annotation; extratum

A:Note: revised physical map for reference I39451
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine

Science 248, 1124-1126, 1990

A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh

A:Reference number: I39453; PMID:90260653; PMID:2111584

A:Accession: I39453

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 656-737 <LEV>

A:Cross-references: GB:M37896; NID:G178618; PIDD:AAAS1727.1; PID:G178620

A:Note: a mutation with 693-Gln is presented

R:Marrelli, J.; Farlow, M.; Ghetti, B.; Benson, M.D.

Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer

A:Reference number: I59562; PMID:92022553; PMID:1925564

A:Accession: I59562

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 689-716, 'F', 718-737 <MUR>

A:Cross-references: GB:S57665; NID:G236720; PIDD:AAAB1991.1; PID:G236721
 R:Kimino, K.; Orr, H.T.; Payant, H.; Wilsman, E.M.; Alonso, M.E.; Pulet, S.M.; Anderson,

Arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
 Am. J. Hum. Genet. 51, 998-1014, 1992

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OM protein - protein search, using sw model

Run on: May 3, 2004, 15:46:00 ; Search time 11 Seconds

(without alignments)
108.874 Million cell updates/sec

Title: US-09-978-178A-7

Perfect score: 116
Sequence: 1 DGDEVEAEAPYEATEERTSIA 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105.5	90.9	751	A4_SAISC	Q95241 s amyloid b
2	105.5	90.9	770	A4_HUMAN	P05067 h amyloid b
3	105.5	90.9	770	A4_MACPA	P53601 m amyloid b
4	105.5	90.9	770	A4_PIG	P79307 s amyloid b
5	105.5	90.9	770	A4_RAT	P08592 r amyloid b
6	102.5	88.4	770	A4_CAVPO	P06495 c amyloid b
7	100.5	86.6	770	A4_MOUSE	P12023 m amyloid b
8	53	45.7	495	GATB_SYNY3	P74215 synchocyst
9	52	44.8	738	YKFA_YEAST	P35732 saccharomyc
10	52	44.0	851	STR8_MOUSE	Q8K031 mus musculu
11	51	44.0	309	HEMZ_AOUAR	Q67083 aquifex aeo
12	51	44.0	339	XAPS_HUMAN	P14320 homo sapien
13	51	44.0	361	APBA_DICDI	P51173 dicystofell
14	51	44.0	563	NAP_HUMAN	Q8WY46 homo sapien
15	51	44.0	563	NAP_MOUSE	Q9CW18 mus musculu
16	50.5	43.5	737	A4_FUGRU	O93279 fugu rubrip
17	49	42.2	606	CENB_CRIGR	P48988 cricetulus
18	49	42.2	671	CHS5_YEAST	O12114 saccharomyc
19	49	42.2	731	DAXX_RAT	O8V1B2 rattus norv
20	48	41.4	407	IE68_HSVSA	O01042 herpesviru
21	48	41.4	493	ECX1_METMA	O8PT88 methanosarc
22	48	41.4	675	SG1_RAT	O35314 rattus norv
23	48	41.4	687	NPHI_MOUSE	C9QY75 mus musculu
24	48	41.4	924	CC13_YEAST	P32797 saccharomyc
25	47.5	40.9	372	MK11_HUMAN	O15759 homo sapien
26	47	40.5	244	1431_ECHGR	O3U408 echinococcu
27	47	40.5	244	1431_ECHMU	O24902 echinococcu
28	47	40.5	364	MK11_MOUSE	O9WU11 mus musculu
29	47	40.5	471	SG3_RAT	P47868 rattus norv
30	47	40.5	538	IE3C_EUGGR	P36171 euglena gra
31	47	40.5	544	NEL_XENLA	P35616 xenopus lae
32	47	40.5	548	IF37_HUMAN	O15371 homo sapien
33	47	40.5	587	RGP1_HUMAN	P46060 homo sapien

34	46.5	40.1	127	1	YHHH_ECOLI	P28911 escherichia
35	46	39.7	317	1	MTX1_MOUSE	P47802 mus musculu
36	46	39.7	370	1	CC37_CABEL	O02108 caenorhabdi
37	46	39.7	423	1	IRK6_HUMAN	P48051 homo sapien
38	46	39.7	542	1	P2CG_MOUSE	O61074 mus musculu
39	46	39.7	587	1	CN39_HUMAN	O8N1B7 homo sapien
40	46	39.7	676	1	SS21_HUMAN	O96M7 homo sapien
41	46	39.7	736	1	DAXX_CERAE	O18805 cercopithec
42	46	39.7	739	1	VNUC_EBOG4	Q9QCE9 ebola virus
43	46	39.7	739	1	VNUC_EBOZ5	Q72142 ebola virus
44	46	39.7	739	1	VNUC_EBOZM	P18272 ebola virus
45	46	39.7	740	1	DAXX_HUMAN	Q9UER7 homo sapien

ALIGNMENTS

RESULT 1
A4_SAISC STANDARD; PRT; 751 AA.
AC Q95241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
(Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
secretase C-terminal fragment 50); C31].
GN APP.
OS Sahitri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
CX NCBI_TaxID=9521;
RN [1]
RP
RC
RT TISSUE=Kidney, and Liver;
RX MEDLINE=96108492; PubMed=8532114;
RA Levy E., Amorim A., Frangione B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with
cerebral amyloid angiopathy.";
RT Neurobiol. Aging 16:805-808(1995).
CC -I- FUNCTION: Functions as a cell surface receptor and performs
physiological functions on the surface of neurons relevant to
neutite growth, neuronal adhesion and axonogenesis. Involved in
cell mobility and transcription regulation through protein-protein
interactions (By similarity). Can promote transcription activation
through binding to APBB1/Tip60 and inhibit Notch signaling through
interaction with Numb (By similarity). Couples to apoptosis-
inducing pathways such as those mediated by G10 and JIP (By
similarity). Inhibits G10 alpha Arpase activity (By similarity).
Acts as a kinase I membrane receptor, mediating the axonal
transport of beta-secretase and presenilin 1 (By similarity). May
be involved in copper homeostasis/oxidative stress through copper
ion reduction. In vitro, copper-metalated APP induces neuronal
death directly or is potentiated through Cu(II)-mediated low-
density lipoprotein oxidation (By similarity). Can regulate
neutite outgrowth through binding to components of the
extracellular matrix such as heparin and collagen I and IV (By
similarity). The splice isoforms that contain the BP1 domain
possess protease inhibitor activity (By similarity).
CC -I- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
with metal-reducing activity. Bind transient metals such as
copper, zinc and iron (By similarity).
CC -I- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
peptides, including C31, are potent enhancers of neuronal
apoptosis (By similarity).
CC -I- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
cytoplasmic proteins, including APBB family members, the APBA
family, MAPK3p1, and SHC1, Numb and Dab1 (By similarity). Binding
to Dab1 inhibits its serine phosphorylation (By similarity). Also

interacts with GPCR-like protein BPP, FPR1, APPB1, IBI, KNS2 (via its TPR domain) (By similarity), APPB2 (via BASS) and DBB1. In vitro, it binds MAPT via the MT-binding domain (By similarity). Associates with microtubules in the presence of APP and in a kinesin-dependent manner (By similarity). Cell surface SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(58) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).

ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=APP70;
IsoId=Q95241-1; Sequence=Displayed;
Name=APP695;
IsoId=Q95241-2; Sequence=Not described.

-1- DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).

-1- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

-1- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields p3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/histatin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity).

-1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

-1- PTM: N- and O-glycosylated (By similarity).

-1- PTM: Phosphorylation on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

-1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity). Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

-1- SIMILARITY: Belongs to the APP family.

-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL; S81024; AAD14347.1; -
DR HSSB; P05067; 1AAP.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; A4-APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PR000222; Kunitz_BPTI; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW Coated pits; Neutrone; Heparin; Glycoprotein; Phosphorylation;
KW Zinc; Signal; Transmembrane; Amyloid; Alternative splicing.
KW Proteoglycan; Amyloid; Alternative splicing.
FT SIGNAL 1 17
FT CHAIN 18 751
FT CHAIN 18 688
FT CHAIN 18 652
FT CHAIN 653 751
FT CHAIN 653 694
FT CHAIN 653 692
FT CHAIN 659 751
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FT CHAIN 693 751
FT CHAIN 695 751
FT CHAIN 702 751
FT CHAIN 721 751
FT CHAIN 18 680
FT DOMAIN 681 704
FT TRANSMEM 705 751
FT DOMAIN 96 110
FT DOMAIN 181 188
FT DOMAIN 291 341
FT DOMAIN 316 344
FT DOMAIN 363 428
FT DOMAIN 504 521
FT DOMAIN 713 732
FT DOMAIN 230 260
FT DOMAIN 274 280
FT SITE 144 144
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FT SITE 738 741
FT SITE 740 743

REACTIVE BOND.
C99 (POTENTIAL).
BETA-AMYLOID PROTEIN 42 (POTENTIAL).
BETA-AMYLOID PROTEIN 40 (POTENTIAL).
C83 (POTENTIAL).
P3 (42) (POTENTIAL).
P3 (40) (POTENTIAL).
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P3 (42) (POTENTIAL).
P3 (40) (POTENTIAL).
GAMMA-CTF (59) (POTENTIAL).
GAMMA-CTF (57) (POTENTIAL).
GAMMA-CTF (50) (POTENTIAL).
G31 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
HEPARIN-BINDING (BY SIMILARITY).
ZINC-BINDING (BY SIMILARITY).
BPTI/KUNITZ INHIBITOR.
HEPARIN-BINDING (BY SIMILARITY).
HEPARIN-BINDING (BY SIMILARITY).
COLLAGEN-BINDING (BY SIMILARITY).
INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
ASP/GLU-RICH (ACIDIC).
POLY-THR.
REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
REACTIVE BOND.
C99 (POTENTIAL).
BETA-AMYLOID PROTEIN 42 (POTENTIAL).
BETA-AMYLOID PROTEIN 40 (POTENTIAL).
C83 (POTENTIAL).
P3 (42) (POTENTIAL).
P3 (40) (POTENTIAL).
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ZINC-BINDING (BY SIMILARITY).
BPTI/KUNITZ INHIBITOR.
HEPARIN-BINDING (BY SIMILARITY).
HEPARIN-BINDING (BY SIMILARITY).
COLLAGEN-BINDING (BY SIMILARITY).
INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
ASP/GLU-RICH (ACIDIC).

Query Match 90.9%; Score 105.5; DB 1; Length 751;
 Best Local Similarity 95.8%; Pred. No. 1.3e-06;
 Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

1 DGDVEEERAEPEYEATERETSTIA 23
 |||||

250 DGDVEEERAEPEYEATERETSTIA 273

RESULT 2
 A4 HUMAN STANDARD; PRT; 770 AA.
 ID_1 A4 HUMAN
 AC P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;
 AC Q16019; Q16020; Q9B138; Q9UCA9; Q9UCB6; Q9UCB8; Q9UCB9; Q9UCD1; Q9UC58;
 DT 13-AUG-1987 (Rel. 05; Created)
 DT 01-NOV-1991 (Rel. 20; Last sequence update)
 DT 15-MAR-2004 (Rel. 43; Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
 nexin-II) (PN-II) (APP1) (Pre4) [Contains: Soluble APP-alpha (S-APP-
 alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
 P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59) (Gamma-
 secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
 (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
 (AID(50)); C31].
 DE (Amyloid intracellular domain 50) (AID(50)); C31].
 GN APP OR A4 OR AD1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87144572; PubMed=2881207;
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
 RA Graeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
 RT cell-surface receptor.";
 RL Nature 325:733-736(1987).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=86122639; PubMed=2893289;
 RA Ponte P., Gonzalez-Dewhilt P., Schilling J., Miller J., Hsu D.,
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
 RA Cordell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine
 RT proteinase inhibitors.";
 RL Nature 331:525-527(1988).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RX MEDLINE=89128427; PubMed=2783775;
 RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The Pre4(65) precursor protein of Alzheimer's disease A4 amyloid
 RT is encoded by 16 exons.";
 RL Nucleic Acids Res. 17:517-522(1989).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM APP770).
 RX MEDLINE=90236318; PubMed=2110105;
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene.";
 RL Gene 87:257-263(1990).
 RN [5]
 RP ERRATUM, AND REVISIONS.
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
 RL Gene 102:291-292(1991).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM I-APP733).

RC TISSUE=Leukocyte;
 RX MEDLINE=92268136; PubMed=1587857;
 RA Koenig G., Moening U., Czech C., Prior R., Banati R.,
 RA Schreiter-Gaesser U., Bauer J., Masters C.L., Beyreuther K.;
 RT "Identification and differential expression of a novel alternative
 RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
 RT leukocytes and brain microglial cells.";
 RL J. Biol. Chem. 267:10804-10809(1992).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM APP770).
 RX MEDLINE=97263807; PubMed=9108164;
 RA Hattori M., Teukahara F., Furuhata Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM APP639).
 RC TISSUE=Brain;
 RX MEDLINE=22744650; PubMed=12859342;
 RA Tang K., Wang C., Shen C., Sheng S., Rayid R., Jing N.;
 RT "Identification of a novel alternative splicing isoform of human
 RT amyloid precursor protein gene, APP639.";
 RL Eur. J. Neurosci. 18:102-108(2003).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM APP305).
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang U., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Garman R.D., Mullaly S.J.,
 RA Raha S.S., Longellano N.A., Peters G.J., Abramson R.D., Bouffard G.G.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Maitra W.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [10]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [11]
 RP ERRATUM, AND REVISIONS.
 RA Mita S., Sadlock J., Herbert J., Schon E.A.;
 RL Nucleic Acids Res. 16:11402-11402(1988).
 RN [12]
 RP SEQUENCE OF 1-75 FROM N.A.
 RX MEDLINE=89165870; PubMed=2538123;
 RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
 RT "Characterization of the 5'-end region and the first two exons of the
 RT beta-protein precursor gene.";
 RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
 RN [13]
 RP SEQUENCE OF 18-50.
 RC TISSUE=Fibroblast;
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";

RL J. Biol. Chem. 262:8508-8514(1987).
RN [14]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=89346754; Pubmed=2569763;
RA de Sauvage F., Octave J.N.;
RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
RT secreted protein.";
RL Science 245:651-653(1989).
RN [15]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87231971; Pubmed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [16]
RP SEQUENCE OF 286-366 FROM N.A.
RX MEDLINE=88122640; Pubmed=2893290;
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Valla-Komaroff L.,
RA Guehla J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease.";
RL Nature 331:528-530(1988).
RN [17]
RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122641; Pubmed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
RL Nature 331:530-532(1988).
RN [18]
RP SEQUENCE OF 507-770 FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=88124954; Pubmed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [19]
RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
RX MEDLINE=96139497; Pubmed=8576160;
RA Behrer D., Hesse L., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RT mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [20]
RP SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717; AD ILE-717
RP AND AD GLY-717.
RX MEDLINE=93236601; Pubmed=8476439;
RA Demian R.B., Rosenczwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
RN [21]
RP SEQUENCE OF 656-737 FROM N.A.
RX MEDLINE=89392030; Pubmed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [22]
Query Match 90.9%; Score 105.5; DB 1; Length 770;
Best Local Similarity 95.8%; Pred. No. 1.4e-06;
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
CY 1 DGDVEEFA-RPYEATRTTSIA 23
|||||||

DB 250 DGDVEEFA-RPYEATRTTSIA 273
RESULT 3
ID A4 MACFA STANDARD; PRT; 770 AA.
AC P53601; Q95KN7;
AD 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein homolog) (Contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE secretase C-terminal fragment 50); C31).
GN APP.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC TISSUE=Cerebellum;
RX MEDLINE=91273117; Pubmed=1905108;
RA Podlasky M.B., Tolian D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease.";
RL Am. J. Pathol. 138:1423-1435(1991).
CC -|- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP (By
CC similarity). Inhibits G(I) alpha APPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction. In vitro, copper-metalated APP induces neuronal
CC death directly or is potentiated through Cu(I)-mediated low-
CC density lipoprotein oxidation (By similarity). Can regulate
CC neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity). The splice isoforms that contain the BPT1 domain
CC possess protease inhibitor activity (By similarity).
CC -|- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).
CC -|- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -|- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APPB family members, the APBA
CC family, MAPK8IP1, and SHC1. Numb and Dab1 (By similarity). Also
CC interacts with GPCR-like protein BPP, FPR1, APPBP1, IRI, KNS2
CC (via its TTP domains) (By similarity), APPBP2 (via BASS) and DDB1.
CC In vitro, it binds MAPT via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of ATP
CC and in a kinesin-dependent manner (By similarity).
CC -|- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC maturation occurs (O-glycosylated and sulfated). After alpha-
CC secretase cleavage, soluble APP is released into the extracellular
CC space and the C-terminal is internalized to endosomes and

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 3, 2004, 15:49:35 / Search time 39 Seconds
(Without alignments)
186.075 Million cell updates/sec

Title: US-09-978-178A-7
Perfect score: 116
Sequence: 1 DGDVEEAEAPYEATERTTTSA 23

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPTREMBL_25:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_podent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102.5	88.4	160	11	Q9QZ78
2	96.5	83.2	693	13	Q98SG0
3	96.5	83.2	695	13	Q98SR8
4	96.5	83.2	695	13	Q7ZXQ0
5	96.5	83.2	747	13	Q91963
6	96.5	82.8	534	13	Q93296
7	96	82.8	569	13	Q9PVL1
8	96	82.8	695	13	Q9DGJ8
9	96	82.8	751	13	Q9DGJ7
10	57	49.1	247	16	Q8ZUT1
11	57	49.1	276	13	P79780
12	53	45.7	477	5	O17729
13	53	45.7	2192	5	Q81BW7
14	52	44.8	766	12	Q9DMF7
15	52	44.8	798	5	O45181
16	52	44.8	866	10	Q9M019

17	52	44.8	1469	5	Q9V953	Q9V953 drosophila
18	51	44.0	224	3	Q02416	Q02416 pneumocysti
19	51	44.0	361	5	Q86AD3	Q86AD3 dictyosteli
20	51	44.0	378	16	Q821X5	Q821X5 streptomyce
21	51	44.0	455	3	Q94548	Q94548 schizosacch
22	51	44.0	563	11	Q80X64	Q80X64 mus musculu
23	50	43.1	72	13	Q800R6	Q800R6 litorea cae
24	50	43.1	189	16	Q9KAJ6	Q9KAJ6 bacillus ha
25	50	43.1	197	10	Q24124	Q24124 nicotiana t
26	50	43.1	248	10	Q9LRH2	Q9LRH2 rapanus sa
27	50	43.1	699	13	Q57394	Q57394 narke japon
28	50	43.1	897	5	O17336	O17336 caenorhabd
29	50	43.1	2658	5	Q8T5G0	Q8T5G0 plasmodium
30	49	42.2	78	2	Q8PMQ4	Q8PMQ4 haemophilus
31	49	42.2	94	17	Q8TKJ9	Q8TKJ9 methanosarc
32	49	42.2	151	10	Q9FM68	Q9FM68 oryza sativ
33	49	42.2	161	10	Q9FM07	Q9FM07 oryza sativ
34	49	42.2	161	10	Q7XCX0	Q7XCX0 oryza sativ
35	49	42.2	471	4	Q86XD1	Q86XD1 homo sapien
36	49	42.2	480	5	Q9NAV6	Q9NAV6 plasmodium
37	49	42.2	521	16	Q8A9P0	Q8A9P0 bacteroides
38	49	42.2	694	5	Q9VVB6	Q9VVB6 drosophila
39	49	42.2	699	10	O64525	O64525 arabidopsis
40	49	42.2	1038	11	Q80Z27	Q80Z27 mus musculu
41	49	42.2	1050	11	Q8CCV0	Q8CCV0 mus musculu
42	49	42.2	1182	11	O08996	O08996 mus musculu
43	49	42.2	1188	11	P97500	P97500 mus musculu
44	49	42.2	1211	11	Q8CHB4	Q8CHB4 mus musculu
45	49	42.2	1226	10	Q84VE4	Q84VE4 oryza sativ

ALIGNMENTS

RESULT 1	ID	Q9QZ78	PRELIMINARY;	PRT;	160 AA.
AC	Q9QZ78	01-MAY-2000 (Tremblrel. 13, Created)			
DT	01-MAY-2000	(Tremblrel. 13, Last sequence update)			
DT	01-JUN-2003	(Tremblrel. 24, Last annotation update)			
DE		Putative amyloid protein (Fragment).			
OS		Cavia sp.			
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX		Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.			
NC		NCBI_TaxID=10143;			
RP		SEQUENCE FROM N.A.			
RC		TISSUE=Lens;			
RA		Frederikse P.H., Carper D., Farnsworth J.P., Zigler J.S.;			
RT		"Piton and Alzheimer precursor protein expression in a hereditary			
RT		guinea pig cataract."			
RL		Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL	AF197164; AAF08934.1; -			
DR	HSSP	P05067; IAA.			
DR	GO	GO:0004867; F:serine protease inhibitor activity; IEA.			
DR	InterPro	IPR002223; Kunitz_BPTI.			
DR	Pfam	PF00014; Kunitz_BPTI; 1.			
DR	PRINTS	PR00759; BASICYPASE.			
DR	PRODom	PD000222; Kunitz_BPTI; 1.			
DR	SMART	SM00131; KU; 1.			
DR	PROSITE	PS00280; BPTI_KUNITZ_1; 1.			
DR	PROSITE	PS0279; BPTI_KUNITZ_2; 1.			
KW		Protease inhibitor; Serine protease inhibitor.			
FT		NON_TER			
FT		NON_TER			
SC		SEQUENCE			
		160 AA; 17424 MW; 9F28C3E92E7F47C1 CRC64;			
QY		Query Match	88.4%;	Score 102.5;	DB 11; Length 160;
		Best Local Similarity	91.7%;	Pred. No. 4,1e-07;	
		Matches	22;	Conservative	1; Mismatches 0; Indels 1; Gaps 1;
					1 DGDVEEAEAPYEATERTTTSA 23

Db 26 DGDVEEFAEPEYEATERTTSTA 49

RESULT 2

ID Q98SG0 PRELIMINARY; PRT; 693 AA.
AC Q98SG0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Beta-amyloid precursor protein A.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
OX [1]
RN SEQUENCE FROM N.A.
RP Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
University of Nijmegen, Nijmegen, Netherlands.
DR EMBL; AJ298150; CAC37193.1; -
DR HSP; P05067; I123.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_EXTRA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR Signal.
KM SIGNAL.
FT SIGNAL.
SQ SEQUENCE 693 AA; 78568 MW; CARIPE55CLAB653 CRC64;
POTENTIAL.
Query Match 83.2%; Score 96.5; DB 13; Length 693;
Best Local Similarity 87.5%; Pred. No. 1.5e-05;
Matches 21; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 DGDVEEFAEPEYEATERTTSTA 23
DB 248 DGDVEEFAEPEYEATERTTSTA 271
RESULT 3
ID Q98SF9 PRELIMINARY; PRT; 695 AA.
AC Q98SF9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Beta-amyloid precursor protein B.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
OX [1]
RN SEQUENCE FROM N.A.
RP Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
University of Nijmegen, Nijmegen, Netherlands.
DR EMBL; AJ298151; CAC37194.1; -
DR HSP; P05067; I123.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_EXTRA.
DR InterPro; IPR001255; Beta-APP.

DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KM SIGNAL.
FT SIGNAL.
SQ SEQUENCE 695 AA; 78803 MW; DC14EB02AFB0204A CRC64;
POTENTIAL.
Query Match 83.2%; Score 96.5; DB 13; Length 695;
Best Local Similarity 87.5%; Pred. No. 1.5e-05;
Matches 21; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 DGDVEEFAEPEYEATERTTSTA 23
DB 249 DGDVEEFAEPEYEATERTTSTA 272
RESULT 4
ID Q7ZXQ0 PRELIMINARY; PRT; 695 AA.
AC Q7ZXQ0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
OX [1]
RN SEQUENCE FROM N.A.
RP Tissue=Embryo;
RC Klein S.; Strauberg R.;
RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC044324; AAH44324.1; -
DR EMBL; BC044324; AAH44324.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_EXTRA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KM Hypothetical protein.
SQ SEQUENCE 695 AA; 78803 MW; C1BD8AAC3356B05 CRC64;

Query Match 83.2%; Score 96.5; DB 13; Length 695;
Best Local Similarity 87.5%; Pred. No. 1.5e-05;
Matches 21; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 DGDVEEFAEPEYEATERTTSTA 23
DB 249 DGDVEEFAEPEYEATERTTSTA 272
RESULT 5
ID Q91963 PRELIMINARY; PRT; 747 AA.
AC Q91963;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE APP747.
GN APP747.
OS Xenopus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae.